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Estimating Prevalence of Injecting Drug Users and Associated Heroin-Related Death Rates in England Using Regional Data and Incorporating Prior Information

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Summary. Injecting drug users (IDUs) have a direct social and economical impact, yet can typically be regarded as a hidden population within a community. We estimate the size of the IDU population across the nine different Government Office Regions of England in 2005/6 using capture-recapture methods with age (ranging from 15-64) and gender as covariate information. We consider a Bayesian model-averaging approach using log-linear models, where we are able to include explicit prior information within the analysis in relation to the total IDU population (elicited from the number of drug-related deaths and injectors' drug-related death rates). Estimation at the regional level allows for regional heterogeneity with these regional estimates aggregated to obtain a posterior mean estimate for the number of England's IDUs of 195840 with 95% credible interval (181700, 210480). There is significant variation in the estimated regional prevalence of current IDUs per million of population aged 15-64; and in injecting drug-related death rates across the gender $\times$ age cross-classifications. The propensity of an IDU to be seen by at least one source also exhibits strong regional variability with London having the lowest propensity of being observed (posterior mean probability of 0.21) and South West the highest propensity (posterior mean of 0.46).

Keywords: Drug-related deaths; Log-linear models; Population size; Injecting drug users; Model-averaging; Prior information

1. Introduction

We focus on estimating the prevalence in 2005/6 of current injecting drug users (IDUs) mainly of opiates in England, and at the Government Office Region level when cross-classified across gender and age (15-34, 35-64). England's population of injectors rose epidemically in the (late) 1980s (de Angelis *et al*, 2004). Opiate substitution therapy (OST)

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was introduced to reduce injection-related harms and to promote off-injecting. Quality assurance in methadone prescribing was achieved between 2000 and 2004 (see Strang *et al* (2010)). A major public health reason to engage injectors in methadone-substitution therapy is to reduce their risks of blood-borne virus transmission and drug-related death (DRD). Methadone clients may continue to inject but, typically, their number of injections of illicit heroin reduces considerably (Hutchinson *et al*, 2000). Estimating the number of current IDUs at the regional and national levels (cross-classified by gender and age) permits the estimation of the injecting DRD rate by taking the ratio of the corresponding number of deaths attributed to injectors (namely heroin-related deaths, HRDs) with the estimated population size of IDUs.

Sudden deaths (which include DRDs) in individuals within the UK are almost always subject to a post-mortem examination to determine the cause of death. Toxicology tests are conducted to identify illicit drugs within the system. Because there is no standardised protocol for conducting or reporting the toxicology of DRDs, there may be some heterogeneity in recording such deaths. Official statistics do not document whether the deceased had a history of injection drug use, let alone whether s/he was a current injector, and so we cannot know which opiate-related DRDs occurred in current injectors. (Not all opiate-related DRDs occur in injectors, but the majority does). It is also possible for a death to be recorded as a DRD even though the drug(s) made no significant contribution to the death, but these cases are likely to be very few for opiate-related deaths. Thus, as a reasonable approximation, we shall count, or attribute, all HRDs (but no methadone-only DRDs) as having occurred in current IDUs. We use the term injecting DRD rate to denotes HRDs per 100 current injectors.

In order to obtain estimates of the number of IDUs we use capture-recapture methods. For closed populations, capture-recapture methods have a long history in both ecological (Otis *et al*, 1978) and epidemiological (Fienberg, 1972) applications. For an overview of the use of capture-recapture methods in epidemiology see, for example, Hook and Regal (1995) and Chao *et al* (2001) with recommendations on the use of such methods presented by Hook and Regal (1999, 2000). Within epidemiology, capture-recapture studies involve collating data across a series of different data sources. Each source records all individuals in the target population observed by that source. Individuals are uniquely identifiable which allows the construction of a contingency table wherein each cell entry corresponds to the number of individuals observed by each distinct combination of sources. However, there is an unobservable cell corresponding to the number of individuals who belong to the target population but were not observed by any source. Thus, failing to estimate this cell entry can significantly underestimate the true target population size, particularly with difficult to reach populations. To estimate the unobservable cell, a model is fitted to the observed data. Capture-recapture studies have been used in a variety of situations including for the estimation of hidden populations (Mastro *et al*, 1994; Frischer *et al*, 1993; Beynon *et al*, 2001; King *et al*, 2009) and disease prevalence (Hook *et al*, 1980; Madigan and York, 1997; Chao *et al*, 2001). We consider the commonly used log-linear models and apply a Bayesian approach that permits the use of a model-averaged estimate of the target population size, thereby accounting for both parameter and model uncertainty (Madigan and York, 1997; King and Brooks, 2001a).

Additional covariate information is often collected corresponding to individual characteristics, such as gender, location, age, marital status etc. Individuals with different characteristics may have different propensities to be observed by different combinations of sources (King *et al*, 2009). Covariates can be introduced as additional factors within the analysis

to account for covariate heterogeneity (Tilling and Sterne, 1999; Tilling *et al*, 2001). For the nine Government Office Regions of England, we adopt a similar approach to King *et al* (2005) by considering two demographic characteristics, each with two levels: gender and age-group, (15-34 years, 35-64 years), by which DRDs are also cross-classified. The break between the different age-groups is chosen since 35+ years is one of the preferred age groups for reporting injecting prevalence estimates at the European Monitoring Centre for Drugs and Drug Addiction. This age group also corresponds with the aging of young initiates into England's injector epidemic from the mid to late 1980s to be in the (35-64) age group in 2005 and beyond. In addition, we note that there is interest in the heroin-related death-rates per 100 current IDUs and the 35+ age-group can represent 15+ years of injecting. We do not include the region itself as a discrete covariate, but analyse the regional data independently of each other. This permits a direct comparison of important interactions identified for each region. Of particular interest is not only the estimates of IDUs within and across regions, but also injectors' HRD rates. We use expert prior information on the injecting DRD rate, combined with information on the regional number of HRDs, to elicit an informative prior on the total number of injectors. The HRDs are themselves provided across the different covariate levels, permitting the estimation of injecting DRD rates for the different joint covariate levels.

In Section 2 we describe the capture-recapture data and introduce the notation that we use before describing the Bayesian approach that we implement to analyse the data in Section 3. Section 4 presents the results, with particular focus on the number of IDUs and associated injecting DRD rates. We conclude with a discussion in Section 5.

2. Regional Data

Data used within the capture-recapture analyses were collected nationally across England in the financial year 2005/6. These data can be disaggregated to the Drug Action Team (DAT) area level. In 2005/6, there were 149 DATs in England. For each DAT area, the same four sources were used to identify IDUs uniquely from which we can construct a 2^4 contingency table with a single unknown cell. The four data sources were (1) probation; (2) Drug Intervention Programme (DIP) prison assessments; (3) drug treatment; and (4) DIP community assessments. In order to cross-classify individuals between the different sources the following set of common identifiers was used for each contributing data source: (a) forename initial, (b) surname initial, (c) gender and (d) date of birth. For each source, only individuals with all four identifiers known were included. For two recorded cases, if all four identifers were the same (Hay *et al*, 2009), we assumed that they related to the same person either between different sources or duplicated within a single source. Geographical information, such as address, postcode sector or district, was used to allocate area of residence. For further information on the data sources see, for example, Singleton *et al* (2006) and Skodbo *et al* (2007) with particular reference to DIPs.

DIPs are a crime reduction initiative which works across different criminal justice bodies (such as police, prison and probation) and drug treatment services. Assessments which record an individual's current drug injecting status are carried out at various points in their journey through the criminal justice system and into treatment, for example via drug testing while in police custody. The registers are comprehensive in their recording of clients either because they relate to formal justice processes (probation, DIP) or because they are needed for reimbursement (such as treatment numbers). However, for an individual client

to be identified as an IDU it does depend on this characterisation being both disclosed and recorded. In England, there has been major investment in DIPs, both in prisons and in the community, with the aim of engaging in assessment and drug treatment those involved in the criminal justice system who test positive for opiates or cocaine (for further details see Skodbo *et al* (2007)). Regions where connections across services are made successfully would be revealed by the same clients tending to feature on more than one data source and perhaps by lower injecting DRD rates if current injectors are successfully engaged in OST, of which methadone accounted for 83% in England in 2005 (Strang *et al*, 2007).

Notationally, we label the four sources S_1, S_2, S_3 and S_4, using the same order as above. We label each cell in the 2^4 contingency table by $\boldsymbol{k} \in \{0,1\}^4$ which represents the combination of sources that an individual is observed by. For example, cell $\boldsymbol{k} = \{0,1,0,0\}$ corresponds to being observed by only source S_2 (DIP prison assessments). This approach permits the individual identifiers of gender and age-group to be considered as covariate data. We requested that the observed individuals be cross-classified by gender and age-group (15-34 and 35-64) which allowed us to receive four 2^4 regional contingency tables, which can be written as a 2^6 contingency table with each cell corresponding to the number of IDUs that are observed by each combination of four sources for each gender $\times$ age-group classification. These contingency table data were originally calculated at the DAT area level. However, there is a trade-off between the geographical scale used and the amount of information contained in the corresponding area-specific data. Regional estimates (and variability) are themselves of interest, yet to retain a reasonable level of information within the contingency tables for fitting models and obtaining estimates we requested for the DAT contingency table data to be aggregated to the nine Government Office Region levels used in previous Home Office reports (Singleton *et al*, 2006). For each of the nine regional contingency tables at the Government Office level, there are four unknown cell entries, corresponding to the number of individuals not observed by any of the sources for each gender $\times$ age-group classification.

For a given region, we let $\boldsymbol{n}_{obs}$ and $\boldsymbol{n}_{unobs}$ denote the set of observed and unobserved cell entries, respectively, and $\boldsymbol{n} = \{\boldsymbol{n}_{obs}, \boldsymbol{n}_{unobs}\}$. The total number of observed individuals is denoted by n. Further, for each individual region, we let $n_{(g,a)}$ denote the observed number of individuals of gender g in age-group a; and $n_{(g,a):\boldsymbol{k}}$ the number of individuals of gender g in age-group a that belong to cell $\boldsymbol{k} \in \{0,1\}^4$ for $g \in \{M, F\}$ (M = male; F = female) and $a \in \{15-34, 35-64\}$. Thus, $n_{(g,a):\boldsymbol{0}} = n_{(g,a):\{0,0,0,0\}}$ denotes the number of individuals of gender g in age-group a that are not observed (i.e. the missing cell for the given cross-classification). Additionally we let $n_{\boldsymbol{0}} = \sum_{g,a} n_{(g,a):\{0,0,0,0\}}$, denote the total number of unobserved individuals.

We let $N_{(g,a)}$ denote the total number of individuals of gender g in age-group a for $g \in \{M, F\}$ and $a \in \{$15-34, 35-64$\}$; and $\boldsymbol{N} = \{N_{(g,a)} : g \in \{\mathrm{M}, \mathrm{F}\}; a \in \{15-34,$ 35-64$\}\}$, so that,

$$N_{(g,a)} = n_{(g,a)} + n_{(g,a):\boldsymbol{0}} = \sum_{\boldsymbol{k} \in \{0,1\}^4} n_{(g,a):\boldsymbol{k}}.$$

We let $N_{tot} = n + n_{\boldsymbol{0}} = \sum_{g,a} N_{(g,a)}$ denote the total number of IDUs in the given region. To provide a brief summary of the data, we present the observed number of unique individuals identified in each region in Table 1 along with the corresponding number observed for each combination of gender and age (i.e. n and $n_{(g,a)}$ for $g \in \{M, F\}$ and $a \in \{$15-34, 35-64$\}$) for each region.

Table 1. Number of unique IDUs observed in each region and each cross-classification of gender and age.

	Region	Total	Male 15-34	Female 15-34	Male 35-64	Female 35-64
EE	East of England	3408	1574	605	962	267
EM	East Midlands	5717	3365	963	1117	272
L	London	8198	2687	1062	3492	957
NE	North East	4585	2944	858	643	140
NW	North West	11309	4678	1756	3904	971
SE	South East	5444	2605	940	1498	401
SW	South West	8767	4091	1580	2405	691
WM	West Midlands	6627	3886	1081	1332	328
YH	Yorkshire and Humber	11221	6413	2221	2089	498
	England	65276	32243	11066	17442	4525

3. Analysis

The observed contingency table for each region is analysed independently of all other regions. We consider log-linear models initially introduced by Fienberg (1972), where the log of the contingency table cell probabilities are a linear sum of main effects and interaction terms between the sources and/or covariates (and normalised so that the sum of the cell probabilities equals unity). We let $\theta_x^{S_i}$ denote the main effect log-linear terms for source S_i, $i \in \{1,2,3,4\}$ at level $x \in \{0,1\}$ and θ_b^B the main effect log-linear terms for covariate $B \in \{G, A\}$ (G = gender, A = age) for the different levels (i.e. $b \in \{M, F\}$ for $B = G$ and $b \in \{15-34, 35-64\}$ for $B = A$). We restrict the set of possible interactions to that of two-way interactions corresponding to source $\times$ source (6 in total), source $\times$ covariate (8 in total) and covariate $\times$ covariate (only 1) interactions. These interactions remove the independence assumption between the different sources. For example, a two-way interaction between sources S_1 and S_2, implies that being observed by source S_1 (probation) increases or decreases the probability of also being observed by source S_2 (DIP prison assessment), and similarly for all other interactions between sources and/or covariates. Notationally, we let $\theta_{x,y}^{S_i,S_j}$ denote the source $\times$ source interaction between sources S_i and S_j ($i, j \in \{1,2,3,4\}$ and $x, y \in \{0,1\}$); $\theta_{x,b}^{S_i,B}$ the source $\times$ covariate interaction between source $i \in \{1,2,3,4\}$ and covariate $B \in \{G, A\}$ for $x \in \{0,1\}$ and $b \in \{M, F\}$ if $B = A$ and $b \in \{15-34, 35-64\}$ if $B = A$; and $\theta_{b,c}^{G,A}$ the covariate $\times$ covariate interaction for $b \in \{M, F\}$ and $c \in \{15-34, 35-64\}$. For identifiability (and prior consistency, see for example King and Brooks (2001b)), we specify sum to zero constraints over the levels of each source or covariate on each of the log-linear terms. For example, we specify $\theta_0^{S_1} + \theta_1^{S_1} = 0$, and similarly for all other source and covariate main effect terms. Similar constraints are specified on the interaction terms, for example, $\theta_{0,x}^{S_1,S_2} + \theta_{1,x}^{S_1,S_2} = 0$ for $x = 0, 1$.

We let $p_{(g,a):\boldsymbol{k}}$ denote the probability an individual is of gender $g \in \{M, F\}$ in age-group $a \in \{15-34, 35-64\}$ and lies in the contingency table cell $\boldsymbol{k} \in \{0,1\}^4$ relating to the four data sources. The saturated model (in terms of the presence of all main effect and two-way interaction terms) has the log-linear cell probabilities of the form,

$$p_{(g,a):\boldsymbol{k}} \propto \exp\left(\sum_{i=1}^{4} \theta_{k(i)}^{S_i} + \theta_g^G + \theta_a^A + \sum_{i=1}^{3}\sum_{j=i+1}^{4} \theta_{k(i),k(j)}^{S_i,S_j} + \sum_{i=1}^{4} \theta_{k(i),g}^{S_i,G} + \sum_{i=1}^{4} \theta_{k(i),a}^{S_i,A} + \theta_{g,a}^{G,A}\right),$$

where $k(i)$ is the ith element of $\boldsymbol{k}$ (i.e. the value of $\boldsymbol{k}$ corresponding to source S_i). Notationally, we let the probability of not being observed by any source be denoted by $p_{\mathbf{0}} = \sum_{g,a} p_{(g,a):\mathbf{0}}$. Sub-models are obtained by setting the two-way interactions terms to be equal to 0 for all levels. We let the set of log-linear parameters be denoted by $\boldsymbol{\theta}$. Finally, we note that,

$$(\boldsymbol{n}_{obs}, n_{\mathbf{0}})|N_{tot}, \boldsymbol{\theta} \sim \text{Multinomial}(N_{tot}, \boldsymbol{q}_{obs}),$$

where $\boldsymbol{q}_{obs}$ denotes the set of probabilities of the observed cells (i.e. $\boldsymbol{k} \in \{0,1\}^4 \backslash \mathbf{0}$ corresponding to being observed by each combination of sources, excluding not being observed by any source) for each gender $\times$ age-group cross-classification and probability of not being observed (i.e. $p_{\mathbf{0}}$). For further discussion see, for example, King *et al* (2005, 2009) who consider similar models in relation to IDUs in Scotland, with region as an additional two-level factor.

3.1. Bayesian approach

We consider a Bayesian approach and analyse the data from each region independently of all other regions so that, without loss of generality, we condition on a given region. For a given log-linear model, m, (in terms of the log-linear parameters present in the model) we let the corresponding set of log-linear parameters be denoted by $\boldsymbol{\theta}_m$. We then form the joint posterior distribution over the set of log-linear parameters and total number of individuals in each gender $\times$ age-group cross-classification,

$$\begin{aligned}
\pi(N_{tot}, \boldsymbol{\theta}_m|\boldsymbol{n}_{obs}) &\propto f(\boldsymbol{n}_{obs}, n_{\mathbf{0}}|N_{tot}, \boldsymbol{\theta}_m)p(N_{tot}, \boldsymbol{\theta}_m) \\
&\propto \frac{N_{tot}!}{(N_{tot}-n)!} \\
&\quad \times \prod_{g\in\{M,F\}} \prod_{a\in\{15-34,35-64\}} \prod_{\boldsymbol{k}\in\{0,1\}^4\backslash\mathbf{0}} p_{(g,a):\boldsymbol{k}}^{n_{(g,a):\boldsymbol{k}}} \times p_{\mathbf{0}}^{n_{\mathbf{0}}} p(N_{tot}, \boldsymbol{\theta}_m).
\end{aligned}$$

The first terms in the posterior distribution correspond to the Multinomial joint probability mass function of the observed cell entries given the total population count and log-linear parameters (and hence cell probabilities) and $p(N_{tot}, \boldsymbol{\theta}_m) = p(N_{tot})p(\boldsymbol{\theta}_m)$, the prior on the total population count and log-linear parameters that are assumed to be independent of each other. Note that we present an alternative parameterisation in Appendix A which may be of particular interest if there is prior information on the gender $\times$ age-group total population counts. In particular, the gender $\times$ age-group total population counts are specified as model parameters with an associated prior distribution. However, this alternative parameterisation does not permit the estimation of the covariate-only log-linear parameters. Within our analysis, the log-linear interaction terms are of particular interest (including presence/absence of such interactions and if present the sign of the interaction) so that we retain the parameterisation presented above, but in Appendix A discuss the implications of using the alternative parameterisation.

We do not specify the log-linear model *a priori*, in terms of the log-linear interaction terms that are present in the model, but consider a model discrimination approach. We follow the approach of Madigan and York (1997) and King and Brooks (2001a) and extend the posterior distribution to include the model space. In other words, we treat the model itself as a discrete parameter, given the observed data, and form the joint posterior distribution

over both the model and parameter space, denoted by $\pi(N_{tot}, \boldsymbol{\theta}_m, m|\boldsymbol{n}_{obs})$. The (marginal) posterior model probability for model m, given the data, can be expressed in the form,

$$\pi(m|\boldsymbol{n}_{obs}) \propto \int_{\boldsymbol{\theta}_m} \sum_{N_{tot}} \pi(N_{tot}, \boldsymbol{\theta}_m, m|\boldsymbol{n}_{obs}) d\boldsymbol{\theta}_m,$$

where the denominator once again ensures that the sum of the posterior distribution over admissible models is equal to unity. In addition, we are also able to calculate the posterior (model-averaged) distribution of the population sizes, accounting for both parameter and model uncertainty. For example, the posterior model-averaged distribution for the number of IDUs for the total population size is given by,

$$\pi(N_{tot}|\boldsymbol{n}_{obs}) = \sum_m \pi(N_{tot}|\boldsymbol{n}_{obs}, m)\pi(m|\boldsymbol{n}_{obs}),$$

where $\pi(N_{tot}|\boldsymbol{n}_{obs}, m)$ denotes the marginal posterior distribution for N_{tot} under model m.

Model-averaging can also be performed within a classical framework (Buckland et al., 1997; Hook and Regal, 1997). However, identifying the set of models with reasonable support to include can be difficult, particularly for large model spaces. In addition, irrespective of using a Bayesian or classical approach, care should be taken when providing model-averaged point estimates. In particular, in the case where competing models with large support provide very different estimates of the parameter(s) of interest, the corresponding model-averaged point estimate could lie in an area of little or no support. In a Bayesian framework such circumstances can usually be identified in terms of a multi-modal marginal posterior density of the parameter(s), and this may be of interest in itself (see for example King *et al* (2009)). For further general discussion of model-averaging, see for example Chapter 6.5 of King et al. (2009) and Burnham and Anderson (2002).

3.2. Prior expert information

There is external information available that can be combined with expert prior beliefs to provide an informative prior in relation to the total number of IDUs, N_{tot}. In particular, we have independent data relating to the number of DRDs for each region between 2004-2007 and prior beliefs relating to the annual DRD rate for injectors. The totality of DRDs includes those with any combination of heroin/morphine, methadone, cocaine, benzodiazapines and alcohol in their systems at time of death. We make the following decisions regarding the classification of DRDs as pertaining to current injectors in order to obtain an estimate of the proportion of injecting DRDs in each region. We assume that current IDUs are only those with any heroin/morphine in their system (irrespective of any other drugs identified). Note that we do not include methadone-only deaths (i.e. no heroin/morphine identified) in our definition of injecting DRDs since methadone-only DRDs may occur preferentially to those enrolled in OST or to those for whom methadone was not prescribed. Individuals taking a mixture of methadone and heroin/morphine are already identified within the HRDs. The corresponding mean annual number of HRDs from 2004-2007 recorded by year of death (see www.rss.org.uk/policy "Registration of deaths in England and Wales") for each region is provided in Table 2.

To form the prior on the total IDU population size, we couple this information with the prior beliefs relating to the annual injecting DRD rate. We specify a symmetric 90% interval for IDUs' annual injecting DRD rate of (0.3%, 1.2%) with median of 0.6% (this

Table 2. Mean number of heroin-related deaths (HRDs) per year of death for each region using data from the four calender years 2004-2007.

Region	Total	Male 15-34	Female 15-34	Male 35-64	Female 35-64
EE	62.75	21.0	3.75	33.0	5.0
EM	64.75	28.5	4.75	27.0	4.5
L	59.5	22.5	4.25	27.25	5.5
NE	39.25	24.5	3.5	9.5	1.75
NW	124.25	49.0	6.25	56.5	12.5
SE	124.0	52.5	10.0	49.75	11.75
SW	111.75	47.75	10.0	46.75	7.25
WM	79.25	34.25	5.25	33.5	6.25
YH	107.25	61.75	7.0	33.25	5.25
England	772.75	341.75	54.75	316.5	59.75

prior was informed by the analysis of Merrall *et al* (2012) of DRD rate for drug treatment clients in Scotland from 1996-2006 and by Scotland's injectors as analysed by King *et al* (2009)). We note that injecting DRD rates are generally higher for older individuals and for males (Merrall *et al*, 2012; Cornish *et al*, 2010), and it is possible to consider different prior intervals for different cross-classified groups (using an alternative model reparameterisation, as discussed in Appendix A). However, to avoid increased variability of annual estimates, and explicitly to model the gender $\times$ age-group interaction we specify a relatively wide interval for the overall injecting DRD rate.

3.3. Prior distributions

We initially specify priors on the log-linear parameters where we do not have any prior information, before we consider the parameter on which there is some expert prior belief: the IDU population size. We complete the prior specification with the prior model probabilities in terms of the interactions present in each model. For each individual region and each possible log-linear model we follow King and Brooks (2001a) and specify a hierarchical $N(\mathbf{0}, \sigma^2 I)$ distribution on the set of log-linear parameters present in the model and use the noninformative prior $\sigma^2 \sim \Gamma^{-1}(0.001, 0.001)$. This implies that, given a two-way interaction is present in the model, there is an equal prior probability that the interaction is positive or negative. See King *et al* (2005) for an alternative prior specification if there is expert prior belief for a positive or negative interaction.

To represent the expert prior information on the total population size, N_{tot}, we specify a log-Normal prior independently over models, due to the prior information being specified in multiplicative form, which results in a skewed distribution. For example, suppose that for a given region the mean annual number of HRDs is X. We specify a prior on the log of the total number of IDUs for the region to be normally distributed with mean $\log(X/0.6\%)$ (so that the prior median is accurately reflected) and variance 0.1776 (to reflect the specified prior 90% interval).

Finally, we specify a prior over the model space. We define the set of possible models to be those models with a maximum of second-order interaction terms (essentially specifying a prior probability of 0 for all higher-order interaction terms). This allows interactions between two sources, two covariates and one covariate and one source. For example, this permits a two-way interaction between DIP community assessment and drug treatment

data, so that being observed by DIP community assessment makes it more or less likely to be observed within the drug treatment data. Clearly, the aim of DIP community assessment work is to increase the number of individuals receiving treatment, so that a positive interaction is desired. However, as stated above, we specify an equal prior probability on each two-way interaction being positive or negative, given the interaction is present in the model. Similarly, a two-way interaction between gender and drug treatment data would be interpreted as male IDUs being more or less likely (than females) to be receiving treatment for drug addiction.

Considering two-way interactions only significantly reduces the number of possible hierarchical log-linear models and aims to focus on the most important direct interactions between the different sources and/or covariates and retain epidemiologically interpretable models without data-dredging. Without any strong prior information relating to the two-way interactions that may be present we specify a prior probability of 0.5 that each interaction is present in the model, but note that the interactions identified within the analysis are of direct interest particularly in terms of any relationships between the different criminal justice sources and/or drug treatment agencies. The specified prior induces an equal prior probability for each possible model in the set of plausible models.

To assess the sensitivity of the posterior estimates of the number of IDUs on the above prior specification, we conduct a prior sensitivity analysis (see Section 4.4) and compare the results obtained. Firstly, we consider the sensitivity of the posterior with respect to the priors specified on the model parameters, using an uninformative prior specification in the form of a uniform prior on the total population count and standard deviation of the log-linear variance term. Secondly, we remove the restriction of considering only two-way interaction terms and allow all possible hierarchical log-linear models, including for example three-way interactions, with each model equally likely (and note that this increases the prior probability of two-way interactions being present in the model).

3.4. (Reversible jump) Markov chain Monte Carlo algorithm

The posterior distribution is defined over both parameter and model space, so that we implement a reversible jump (RJ) Markov chain Monte Carlo (MCMC) algorithm (Green, 1995) since the posterior distribution is multi-dimensional (as the number of parameters differs between models). The advantage of the reversible jump algorithm is that the Markov chain simultaneously explores the parameter and model space. This means that we do not need to fit each possible model individually. Irrespective of the number of possible models, only a single chain is necessary (though typically as the model space increases, so does the length of the Markov chain needed). Within the algorithm, we use a two-step procedure:

Step 1: Conditional on the model, we cycle through each individual parameter in turn and propose to update the parameter using a Gibbs or Metropolis-Hastings (MH) step (note that we also simulate population counts for each gender $\times$ age-group cross-classification from the posterior conditional distribution);

Step 2: Update the model using a reversible jump step by adding or removing a log-linear interaction term from the model.

We consider each step in turn.

3.4.1. Step 1: Updating the parameters
We update σ^2 using a Gibbs step, since the posterior conditional distribution is of standard form (i.e. inverse Gamma) and a single-update random walk MH algorithm is used for all the other log-linear parameters and total population size. See Brooks (1998) for a general description of these algorithms and King and Brooks (2001a) for the specific application to the log-linear parameters. We note that not only is the total population size of interest, but also the population sizes for each gender $\times$ age-group cross-classification. These can be easily obtained within the MCMC algorithm by simply simulating these population sizes from their posterior conditional predictive distribution at each iteration of the Markov chain. In particular, we have that,

$$\boldsymbol{n}_{unobs}|N_{tot}, \boldsymbol{\theta}, \boldsymbol{n}_{obs} \sim \text{Multinomial}(N_{tot} - n, \boldsymbol{q}_{unobs}),$$

where $\boldsymbol{q}_{unobs} = \{q_{(g,a):unobs} : g \in \{M, F\}, a \in \{15-34, 34-65\}\}$ and,

$$q_{(g,a):unobs} = \frac{p_{(g,a):\mathbf{0}}}{\sum_{g,a} p_{(g,a):\mathbf{0}}}.$$

In other words $q_{(g,a):unobs}$ denotes the probability that an individual is of gender g and in age-group a given that they are not observed within the study.

3.4.2. Step 2: Updating the model
To update the log-linear interaction terms present within the model we use a reversible jump step (Green, 1995). For a single RJ step, we propose to add or remove a single two-way interaction term (since we only consider models with two-way interactions). We choose each log-linear interaction with equal probability. If the parameter is present in the model, we propose to remove the parameter; if it is not in the model, we propose to add the parameter. Suppose that we propose to add a given two-way interaction parameter. We propose a candidate value from a proposal distribution, q, which in this case is a Normal distribution. The corresponding proposal mean is obtained using the posterior mean of the given parameter from a pilot MCMC run in the model containing all two-way interactions. The proposal variance is chosen via pilot-tuning. The corresponding acceptance probability simply reduces to the ratio of the likelihood function using the proposed and current parameter values respectively, multiplied by the ratio of the prior density function to proposal density function for the newly proposed log-linear parameter (the Jacobian is equal to unity). See King and Brooks (2001a) for further details using an analogous approach and Forster *et al* (2012) and Papathomas *et al* (2011) for alternative reversible jump implementations.

For each region, the RJMCMC algorithm is run for a total of 10 million iterations with the first 10% discarded as burn-in. For memory storage purposes the observations are thinned every 5 iterations. Three independent replications using over-dispersed starting points obtained similar results (all with the same interpretation) so that we conclude that the algorithm has sufficiently converged. Additionally, using the Brooks-Gelman-Rubin statistic on the missing cell entries provided no evidence for lack of convergence. The mean acceptance probabilities for adding or removing the log-linear terms lay around 1.5% for each of the different regions (mean values ranged from 0.7% to 2.5%). The mean acceptance values are not high, but this is partially explained by many of the log-linear terms having

either a very high probability of being present or not being present (see Table 4.3), so that removing or adding such terms, respectively, was largely rejected in the reversible jump chain. In other words, taking into account the number of possible models, there was relatively little uncertainty in the parameters present in the model.

4. Results

4.1. Estimating the Number of Injecting Drug Users

Figure 1 provides plots of the prior and (model-averaged) marginal posterior distributions for the number of IDUs in each region. These model-averaged density estimates appears to be uni-modal, so that models with reasonable posterior support appear to provide similar estimates of population size. For regions East Midlands, London, North East, North West, West Midlands and Yorkshire and Humber, the priors generally appear to underestimate the number of IDUs in the different regions. The most significant difference between the prior and posterior distributions is clearly for London with virtually no overlap between the prior and posterior distributions. This would potentially suggest, for these regions, and London particularly, that (i) the number of injecting DRDs is an underestimate and/or (ii) the injecting DRD rate is lower than the prior expert beliefs. We return to this issue below when discussing the posterior injecting DRD rates.

Table 3 provides the posterior estimates for the total population size and each combination of gender $\times$ age-group cross-classifications for each of the regions, in addition to the corresponding population sizes for England (i.e. posterior estimates summed over each region). The posterior mean of the total current injector population for England can be easily calculated as the sum of the posterior means of the estimates for each region. However, the corresponding credible intervals (CIs) at the England level cannot be obtained directly from the credible intervals for each individual region. For example, summing the 2.5% quantiles (used for the lower bound of the 95% credible interval) over all regions will not give the corresponding 2.5% quantile for England (the value obtained would be for a much lower quantile for the total population size for England). We are able to obtain the 95% credible interval at the national level by considering a Monte Carlo approach. Recall that the regional datasets are analysed independently of each other, so that the posterior (marginal) distributions of the population sizes are independent across regions. To obtain a sample observation from the posterior distribution of the population size for England, we simply take a sample observation of the number of IDUs from each region and sum these values. By repeatedly sampling from the set of regional posterior distributions for IDU population sizes, we can obtain, for England, a Monte Carlo estimate for the credible intervals of interest.

From Table 3 we see that three regions (London, North West and Yorkshire and Humber) appear to have significantly higher absolute number of IDUs. In addition, consistently, there is a larger estimated number of males than females in each region for each age-group considered. Overall, the posterior mean ratio of males to females (aggregated to the England level) is 3.22 with corresponding 95% symmetric CI (3.02, 3.38). The posterior mean male to female ratio over the different regions ranges from 2.74 (South West) to 4.19 (East Midlands). Capture propensities also appear to differ between regions, in terms of the proportion of individuals who are observed by at least one source. Injectors' in London have the least propensity of being observed (posterior mean 0.21 with 95% CI (0.16, 0.28)), IDUs in the South West the highest propensity (posterior mean 0.46 with 95% CI (0.40,

Fig. 1. The posterior distribution for the total population size for each region (in black) and the corresponding prior distribution (in grey).

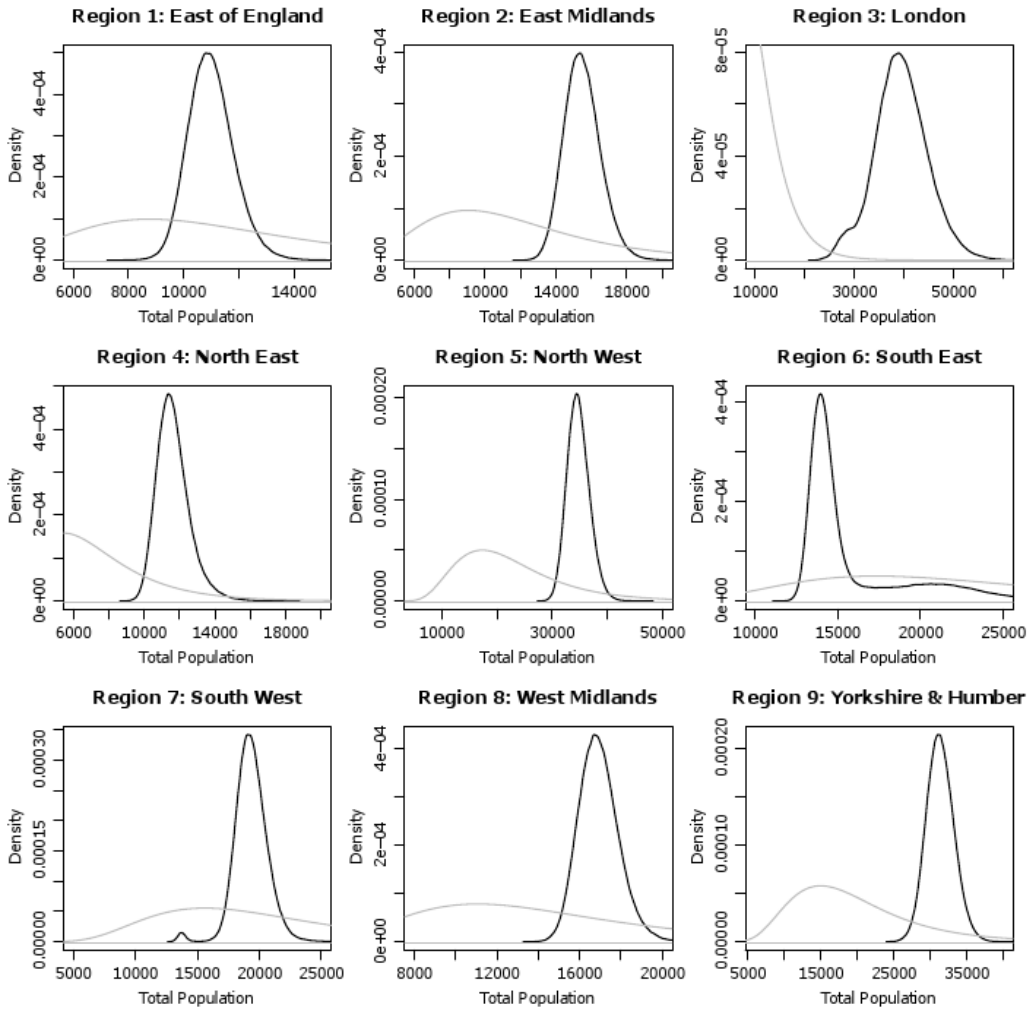

Table 3. Posterior mean and 95% symmetric credible interval (in brackets) for the total number of IDUs in each region and each cross-classification of gender and age and aggregated to the England level using a Monte Carlo approach (rounded to nearest 10).

Region	Total	Male 15-34	Female 15-34	Male 35-64	Female 35-64
EE	11000	5120	1680	3420	780
	(9450, 12680)	(4340, 5950)	(1370, 2000)	(2790, 4050)	(610, 950)
EM	15490	9030	2280	3460	720
	(13540, 17540)	(7860, 10230)	(1860, 2760)	(2950, 4000)	(560, 900)
L	39390	14430	4630	16770	3570
	(27870, 50060)	(10050, 18730)	(3090, 6200)	(11770, 21520)	(2430, 4750)
NE	11650	7350	2220	1680	390
	(9940, 13540)	(6250, 8570)	(1810, 2650)	(1290, 2050)	(280, 490)
NW	34770	13250	5560	12580	3370
	(30920, 38780)	(11810, 14740)	(4890, 6260)	(11120, 14090)	(2930, 3820)
SE	15930	7230	2760	4660	1290
	(12550, 23720)	(5690, 10670)	(2120, 4120)	(3570, 7020)	(960, 1960)
SW	19320	8680	3550	5470	1620
	(16980, 22040)	(7610, 9860)	(2970, 4140)	(4740, 6310)	(1330, 1910)
WM	16930	9480	2890	3580	990
	(15100, 18850)	(8460, 10540)	(2510, 3270)	(3130, 4040)	(820, 1150)
YH	31360	17040	6530	6190	1590
	(27710, 35110)	(15100, 19060)	(5710, 7370)	(5400, 7000)	(1360, 1830)
England	195840	91610	32100	57810	14320
	(181700, 210480)	(85610, 97950)	(29760, 34550)	(52260, 63420)	(12910, 15800)

0.51)). The posterior means for all other regions lay within the range (0.31-0.40).

For comparison with the estimate of the number of IDUs in England in Table 3 by aggregating the posterior regional estimates, we perform a further analysis where we aggregate the raw data across the Government Office Regions and analyse the resulting contingency table using the same Bayesian approach. To analyse these data, we use the same prior beliefs as before, which provide a prior median for the total population size of 128792 with 90% interval (64396, 257583). This lower bound is actually less than the number of observed IDUs (see Table 1). The corresponding posterior mean (rounded to nearest 10) of the total population size is 209820 with 95% symmetric CI of (197930, 222200). Thus, the regionally-derived England estimate (i.e. obtained by aggregating the posterior regional estimates) is generally lower than that obtained when analysing the data without heed to the regional component (although there is some overlap between the credible intervals). If we consider the corresponding estimates for the cross-classifications when aggregating at the data level we obtain posterior means and 95% symmetric CIs (rounded to nearest 10) for males 15-34 of 96440 (90960, 102100); females 15-34 of 36940 (34480, 39430); males 35-64 of 59830 (56190, 63620); and females 35-64 of 16610 (15380, 17810). The posterior estimate for males are fairly consistent with the regionally-derived England estimates in Table 3 (with significant overlap between the credible intervals), but estimates were higher for females. In other words, allowing for heterogeneity at the regional level results in lower estimates of female IDUs.

A previous estimate for England (using the same capture-recapture data but analysed at the DAT level) obtained by Hay *et al* (2009) is significantly lower, with a point estimate of 129980 and 95% confidence interval (125790, 137030), rounded to nearest 10. Estimates

Table 4. Current injector totals set in context by regions' mid-2005 population aged 15-64 and estimated ratio of young to old (i.e. 15-34 to 35-64) for each gender in each region.

Region	mid-2005 populations aged 15-64 (in 1000s)	Posterior mean of current injectors (per 1,000) population aged 15-64 (95% CI)	Posterior mean current injectors to nearest 50 (95% CI)	Posterior mean of male injector ratio by age-group (15-34/35-64) (95% CI)	Posterior mean of female injector ratio by agE-group (15-34/35-64) (95% CI)
EE	3604.0	3.1 (2.6, 3.5)	11000 (9450, 12700)	1.50 (1.32, 1.76)	2.15 (1.83, 2.52)
EM	2839.0	5.5 (4.8, 6.2)	15500 (13550, 17550)	2.61 (2.41, 2.82)	3.17 (2.72, 3.58)
L	5269.0	7.5 (5.3, 9.5)	39400 (27850, 50050)	0.86 (0.76, 0.97)	1.30 (1.13, 1.48)
NE	1686.1	6.9 (5.9, 8.0)	11650 (9950, 13550)	4.40 (3.80, 5.47)	5.85 (4.46, 7.50)
NW	4497.0	7.7 (6.9, 8.6)	34750 (30900, 38800)	1.05 (1.01, 1.10)	1.65 (1.54, 1.77)
SE	5338.0	3.0 (2.4, 4.4)	15950 (12550, 23700)	1.56 (1.45, 1.66)	2.15 (1.92, 2.37)
SW	3252.7	5.9 (5.2, 6.8)	19300 (17000, 22050)	1.59 (1.51, 1.67)	2.20 (2.03, 2.38)
WM	3499.9	4.8 (4.3, 5.4)	16950 (15100, 18850)	2.65 (2.46, 2.83)	2.92 (2.58, 3.32)
YH	3325.7	9.4 (8.3, 10.6)	31350 (27700, 35100)	2.75 (2.61, 2.90)	4.11 (3.76, 4.48)
England	33311.4	5.9 (5.5, 6.3)	195850 (181700, 210500)	1.59 (1.51, 1.67)	2.24 (2.12, 2.36)

aggregated at the Government Office Regions are also generally smaller (with the exception of South East). We return to possible reasons for this apparent discrepancy in Section 4.3 when we discuss in detail the interactions identified for each of the Government Office Regions. Alternatively, using a Bayesian evidence synthesis approach to estimating the prevalence of Hepatitis C virus infections, de Angelis *et al* (2009) provide a posterior median for the current IDU population in 2003 for England and Wales of 217000 with 95% credible interval (157000, 309000), which is broadly consistent with our estimate when taking their inclusion of Wales into account. The same analysis also provided estimates for London and North West, with posterior means of 38000 and 23000 with 95% credible intervals (30000, 48000) and (14000, 38000) respectively, which again appear to be largely consistent with the estimates obtained using only the capture-recapture data here if only because of wide uncertainty. For example, the estimate by de Angelis *et al* (2009) for the North West has a relatively much wider credible interval than does ours. Finally, we note that Hickman *et al* (2004) provided a capture-recapture estimate for London of 34400, for the slightly earlier year of 2001 for those aged 15-44.

Table 4 relates the centrally estimated number of current injectors to regions' mid-2005 population aged 15-64, since the regions differ in population size. England has an estimated

5.9 current injectors per 1,000 of the population aged 15-64 (with 95% symmetric credible interval 5.5-6.3). The estimated injector prevalence is low (posterior mean around 3) in East England and the South East, high (posterior mean around 7.5) in London, the North East and the North West and very high (posterior mean around 9) for Yorkshire and Humberside. However, it is an encouraging sign for London and the North West (with high prevalence rates) that their injector age-group ratios (15-34 to 35-64) are relatively low compared to England as a whole (posterior mean of 1.59 for males; 2.24 for females; and see Millar *et al* (2006) for further detailed discussion of problem drug use in the North West up to 2001). Regions with high injector ratios by age-group may have experienced later diffusion with younger injectors predominating. These regions include East and West Midlands, North East and Yorkshire and Humberside, the last of which is also beset by the largest overall injector prevalence per 1,000 of the population aged 15-64.

4.2. Injecting Drug-related Death Rates

We obtain a sample from the posterior distribution for the injecting DRD rates by taking the ratio of the mean annual number of HRDs (as provided in Table 2) with the total number of IDUs for each gender $\times$ age-group cross-classification at each iteration of the Markov chain. The corresponding posterior mean and symmetric 95% CI of the injecting DRD rates are provided in Table 5. Recall that the prior 90% interval on the injecting DRD rates was (0.3%, 1.2%). We comment first at the England level and observe that the posterior injecting DRD rate is at the lower end of the prior distribution informed by the Scottish analyses. We note that the overall posterior estimate for the injecting DRD rate is lower than that presented by Bloor *et al* (2008) who investigated the "Scottish effect" of higher DRD rates in Scotland compared to England, and offered an estimate for Scotland of 0.8% (with 95% uncertainty interval 0.5%-1.2% using data from 2001-5); our estimated injecting DRD rates for England indeed fall below the lower end of their uncertainty interval. In addition, the injecting DRD rate in England appears to be significantly lower for younger than older injectors: for males, a posterior mean of 0.37% for the younger age-group compared to 0.55% for the older age group with non-overlapping credible intervals; and likewise for females, with posterior means of 0.17% to 0.42% for the younger and older age groups. We note that the previous Scottish analysis of King *et al* (2009), using data from 2003-5, estimated significantly higher injecting DRD rates for the cross-classified groups in Scotland but, unlike this analysis, only identified a lower female injecting DRD rate for young injectors with no gender differential for older injectors. For England, more definitively than for Scotland, we observe that older females' injecting DRD rate is also significantly lower than for older males (posterior mean of 0.42% versus 0.55% with non-overlapping credible intervals). See King *et al* (2009) for further details and results relating to the analyses of the Scottish data. Finally, we note that England's overall injecting DRD rate, as defined by us, appears to be similar to the DRD rate of 0.36% reported by Merrall *et al* (2012) for all Scotland's drug treatment clients in the five years to the end of March 2006, despite this estimate for Scotland relating to problem drug-users who had sought treatment and who included non-injectors.

We now consider the results at the regional level. Comparing the results in Table 5 with the 90% prior interval for injecting DRD rate, it is clear that the London appears to be the most at odds with these prior beliefs, with the upper 97.5% posterior quantiles of injectors' DRD rates lower than 0.3% (the lower 5% prior quantile) for each gender $\times$ age-group. Comparing the prior and posterior distributions of numbers of IDUs in Figure

Table 5. Posterior mean and 95% symmetric credible interval (in brackets) for the injecting DRD rate (as %), in each region and each cross-classification of gender and age.

Region	Total	Male 15-34	Female 15-34	Male 35-64	Female 35-64
EE	0.57	0.41	0.23	0.97	0.65
	(0.49, 0.66)	(0.35, 0.48)	(0.18, 0.27)	(0.80, 1.16)	(0.51, 0.79)
EM	0.42	0.32	0.21	0.79	0.63
	(0.37, 0.47)	(0.28, 0.36)	(0.17, 0.25)	(0.67, 0.90)	(0.48, 0.77)
L	0.15	0.16	0.09	0.17	0.17
	(0.11, 0.20)	(0.11, 0.21)	(0.06, 0.13)	(0.12, 0.22)	(0.11, 0.21)
NE	0.34	0.34	0.16	0.57	0.46
	(0.29, 0.39)	(0.28, 0.39)	(0.13, 0.19)	(0.45, 0.72)	(0.34, 0.60)
NW	0.36	0.37	0.11	0.45	0.37
	(0.32, 0.40)	(0.33, 0.41)	(0.10, 0.13)	(0.40, 0.50)	(0.32, 0.42)
SE	0.81	0.75	0.38	1.11	0.95
	(0.51, 0.97)	(0.48, 0.90)	(0.24, 0.46)	(0.69, 1.35)	(0.58, 1.18)
SW	0.58	0.55	0.28	0.86	0.45
	(0.50, 0.65)	(0.48, 0.62)	(0.24, 0.33)	(0.73, 0.97)	(0.37, 0.53)
WM	0.47	0.36	0.18	0.94	0.64
	(0.42, 0.52)	(0.32, 0.40)	(0.16, 0.21)	(0.82, 1.06)	(0.53, 0.75)
YH	0.34	0.36	0.11	0.54	0.34
	(0.30, 0.38)	(0.32, 0.41)	(0.09, 0.12)	(0.47, 0.61)	(0.28, 0.38)
England	0.40	0.37	0.17	0.55	0.42
	(0.37, 0.42)	(0.35, 0.40)	(0.16, 0.18)	(0.50, 0.60)	(0.38, 0.46)

1 we see very little overlap between these distributions. The significantly higher posterior estimate of the population size (compared to the prior specification) consequently produces the lower estimates of the injecting DRD rates.

For all regions, the lowest injecting DRD rates are for females in the younger age-group (15-34), with many regions having an injecting DRD rate in the lower 5% quantile of the prior interval. Overall, the female injecting DRD rates are generally lower than for the males. The older age-group (35-64) has a higher injecting DRD rate for both males and females, relative to the younger age-group (15-34). This appears to be broadly consistent with other studies showing increased mortality rates for older individuals and males (Cornish *et al*, 2010; Merrall *et al*, 2012).

The difference in the injecting DRD rates across the different regions could be a result of (1) a genuine artefact across the different regions, (2) mis-estimation of the number of IDUs (i.e. the denominator), (3) mis-classification of the number of injecting DRDs (i.e. the numerator) or (4) mis-estimation of the number of IDUs and mis-classification of the number of injecting DRDs. It is not possible to rule out either mis-estimation or mis-classification. As discussed in Section 1 there may be some heterogeneity with respect to the mis-classification of injecting DRDs, for example, in the recording of the presence/absence of heroin/morphine and/or methadone, based on presence of toxicology or based on whether it was implicated in the death. In addition (except for London as we discuss in Section 4.4) the regional estimates obtained are insensitive to the priors specified on the parameters and models, which suggests that significant mis-estimation is unlikely. Thus, assuming that there are some genuine regional differences in the risk of mortality for IDUs, three regions in Table 5 (East of England, South East and South West) had particularly high injecting DRD rates, the first two of which (East of England and South East) can be seen from Table

4 as regions with the lowest prevalence of current injectors per 1,000 of the population aged 15-64.

4.3. Marginal Log-linear Probabilities

The corresponding marginal posterior probability that each covariate is present in the model for each separate region is provided in Table 6. Note that we identify "positive" evidence for a Bayes factor of ≥ 3 for the the presence of an interaction, corresponding to a posterior model probability ≥ 0.75, and "strong" evidence for a Bayes factor of ≥ 20, or posterior probabilities ≥ 0.95 (Kass and Raftery, 1995). There are several points of interest. Multiple interactions are clearly important across all (or the majority of) regions, namely, $S_1 \times S_2$ (probation $\times$ DIP prison data); $S_1 \times S_3$ (probation $\times$ drug treatment data); $S_2 \times G$ (DIP prison data $\times$ gender); $S_4 \times A$ (DIP community assessment data $\times$ age). For all these interactions, the sign of the interaction is consistent across regions. In particular, a decreased probability of being observed by DIP prison data for females; a decreased probability of being observed by DIP community assessment data for the older age group; and positive interactions for $S_1 \times S_2$ and $S_1 \times S_3$, indicating, as we would perhaps expect, an increased probability of being observed within DIP prison data and drug treatment data if an individual is observed within probation (individuals released from prison are often placed on probation and drug treatment can be a requirement of probation).

Similarly there is a set interactions each of which is identified in a majority of regions. These are $S_1 \times S_4$ (probation $\times$ DIP community assessment data for all regions except South East); $S_2 \times S_4$ (DIP prison data $\times$ DIP community assessment data for all regions except South East and South West, though there is posterior uncertainty in the South West); $S_3 \times S_4$ (drug treatment data $\times$ DIP community assessment data for all regions except East England and South East); $S_1 \times A$ (probation $\times$ age for all regions except East England and London); $S_2 \times A$ (DIP prison data $\times$ age for all regions except North East); $G \times A$ (gender $\times$ age identified in all regions except West Midlands). Once more, for the regions where the interaction is identified the sign of the interaction is consistent. We note that the positive interaction $S_3 \times S_4$ (treatment data $\times$ DIP community assessment data), as identified in all regions except East England and South East, is a highly desired cross-linkage via increased uptake of drug treatment for individuals in DIP community assessment programmes.

There are some further discrepancies over the different regions regarding the presence of particular interactions. These include:

- London and Yorkshire and Humber: the only regions to identify the interaction $S_2 \times S_3$ (DIP prison assessment data $\times$ drug treatment data), despite large investment in the DIP initiative to lead to increased drug treatment. As we would expect, when this interaction is identified, it is positive. The lack of identification of this interaction is disappointing for other areas, as there does not appear to be the prison-drug treatment centre links made that are intended.

- London: the only region that identifies the interaction $S_3 \times A$, with older individuals more likely to be observed by the treatment data. However, for this region, the interaction $S_1 \times A$ is not identified whereby, in other regions, fewer younger individuals are identified via source S_1 (probation).

- East of England, East Midlands and London: identify an interaction $S_3 \times G$ (drug treatment data $\times$ gender) but no interaction between $S_4 \times G$ (DIP community assess-

Table 6. Marginal posterior probability for each two-way interaction being present in the model for each region. Recall that S_1 = probation; S_2 = DIP prison assessment data; S_3 = drug treatment data; S_4 = DIP community assessment data; G = gender; and A = age.

Interactions	Region								
Source × Source	EE	EM	L	NE	NW	SE	SW	WM	YH
$S_1 \times S_2$	0.996	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
$S_1 \times S_3$	0.998	1.000	0.951	1.000	1.000	1.000	0.988	1.000	1.000
$S_2 \times S_3$	0.068	0.049	0.994	0.160	0.055	0.281	0.076	0.086	0.981
$S_1 \times S_4$	1.000	1.000	1.000	1.000	1.000	0.486	1.000	1.000	1.000
$S_2 \times S_4$	1.000	0.999	1.000	1.000	1.000	0.095	0.690	1.000	1.000
$S_3 \times S_4$	0.060	1.000	1.000	1.000	1.000	0.330	0.988	1.000	1.000
Source × Covariate									
$S_1 \times G$	0.050	0.168	0.226	0.061	0.997	0.115	0.997	0.995	0.843
$S_2 \times G$	1.000	1.000	0.833	0.985	1.000	0.998	1.000	1.000	1.000
$S_3 \times G$	0.971	0.959	0.953	0.171	0.033	0.039	0.117	0.060	0.031
$S_4 \times G$	0.119	0.470	0.379	0.957	1.000	0.916	1.000	0.955	1.000
$S_1 \times A$	0.657	1.000	0.109	0.816	1.000	0.981	1.000	0.967	0.986
$S_2 \times A$	0.929	1.000	1.000	0.537	1.000	1.000	1.000	1.000	1.000
$S_3 \times A$	0.117	0.054	0.999	0.262	0.026	0.045	0.062	0.061	0.055
$S_4 \times A$	0.993	1.000	1.000	0.998	1.000	1.000	1.000	0.999	1.000
Covariate×Covariate									
$G \times A$	0.997	0.787	1.000	0.867	1.000	0.999	1.000	0.489	1.000

ment data × gender). For these regions, there is an increased probability for females to be observed within drug treatment agencies but no support for the interaction $S_4 \times G$, identified by all other regions, wherein there is a decreased probability of females being observed in DIP community assessment programmes.

- North West, South West, West Midlands and Yorkshire and Humber: the only regions to provide positive support for the interaction $S_1 \times G$ (probation × gender) with a decreased probability of being observed within probation for females.

Finally, we return to the comparison of results obtained within this analysis and those of Hay *et al* (2009), who considered the same data but analysed at the DAT area level. Within their analyses, they did not include the covariate information and considered only the set of log-linear models with a maximum of two source × source interactions (a total of 22 models). Typically, the model with lowest AIC value was chosen (although see Hay *et al* (2009) for more specific details) and the corresponding estimate for total population was as given by the chosen log-linear model. For all Government Office Regions, except South East, the number of source × source interactions identified in our models typically lies between 4 and 6. Further, all of the source × source interactions that are identified with large posterior support for each region have a posterior mean that is positive. Thus, not including such interactions (as for 8 of the 9 regions) results in the decreased estimate of population size obtained by the previous analysis of Hay *et al* (2009), rather than differences being due to the use of the lower DAT area level data or ignoring the gender and age-group covariate information. Conversely, for South East, (where only two source × source interactions are identified with positive support) Hay *et al* (2009) provide an overall estimate and 95% confidence interval of 13270 (10290, 16380), which is reasonably consistent with the estimate provided in Table 2, with both point estimates contained in the alternative

analysis's uncertainty interval but this is not the case for any other region.

4.4. Sensitivity Analyses

We present two sensitivity analyses. The first considers the prior specification on the parameters, while the second considers the prior on the set of possible models. We initially consider the prior specification on the parameters, and the set of models allowing only two-way interaction terms with each possible model equally likely, as in the previous analysis. We specify a Uniform prior on the total population size and set the standard deviation of the log-linear terms to be uniform, with a suitable large upper limit (Gelman, 2006). In particular, we set $\sigma \sim U[0, 100]$. The RJMCMC algorithm is run for each of the different regional contingency tables, and the aggregated England dataset. The posterior distributions obtained for the majority of analyses (all except London) are very similar for those obtained for the previous informative priors (for example, estimated posterior means for the total number of IDUs within 4% of each other and the same interactions are identified as before), suggesting that the posterior distribution in these cases are data-driven. For London, larger estimates are obtained (approximately 19% higher), which suggests that the informative prior specification had some influence on the posterior estimates in this region.

Secondly, we remove the restriction on the models considered within the analysis and allow higher order interactions. We specify an equal prior probability for each possible hierarchical log-linear model, retaining the previous informative priors and run an RJMCMC algorithm for each of the Government Office Regions and for the aggregated England data. We initially discuss the estimates obtained at the England level for both the results aggregated using the regional level data and the results obtained by aggregating at the data level.

The estimated posterior mean of the total number of IDUs (to nearest 1000) obtained by aggregating the estimates obtained from the analyses of the regional data is 191000 with 95% posterior credible interval of (176000, 210000), slightly lower than the previously obtained estimate using only two-way interactions, but with large overlap between the credible intervals. Analysis of the data aggregated to the England level before model fitting obtains a posterior mean total estimate (to nearest 1000) of 211000 with 95% symmetric CI (198000, 224000). This is slightly higher than the estimate obtained when considering the regional data but with overlapping credible intervals. We note that there is positive posterior support for only one three-way interaction, $S_1 \times S_2 \times G$ (probation $\times$ DIP prison data $\times$ gender), with females having an increased probability of being observed by both sources.

We now consider the results obtained at the regional level. For all the regional level datasets, except London, the estimated posterior means for the cross-classified (and total) number of IDUs all lie within 10% of the results obtained using only two-way interaction terms (with the majority lying within 5%), although there are some differences with regard to interactions observed to be present. Unsurprisingly, the 95% posterior credible intervals are generally slightly wider, representing the additional model uncertainty. For London, the estimated total number of IDUs is significantly lower, with a posterior mean of 26430 with 95% symmetric credible interval (17490, 42830), which still has significant overlap with the previous estimate. The decrease in estimate (approximately 30%) is consistent across the gender $\times$ age cross-classifications, and directly leads to the reduced overall estimate for England. The reason for this lower estimate in London appears to be related to the identification of a three-way interaction term between sources $S_2 \times S_3 \times S_4$ (DIP prison $\times$

drug treatment × DIP community assessment data), but note that this interaction is not identified within any other region. In particular, if an individual is identified by both forms of DIP data (or not observed by either of these sources), they have an increased probability of being observed in drug treatment.

Allowing this interaction to be present removes the presence of the two-way interaction between probation and drug treatment data within London (which is clearly identified as being present in all other regions). Alternatively, for the North West, South West, West Midlands and Yorkshire and Humber regions, the three-way interaction between criminal justice sources $S_1 \times S_2 \times S_4$ (probation × DIP prison × DIP community assessment data) was identified, with an increased probability of being observed by all three sources. Further three-way interactions identified were $S_1 \times S_4 \times A$ (DIP prison data × DIP community data × age) for South East (for the older age group a reduced probability of being observed by both sources); $S_1 \times S_4 \times G$ (probation × DIP community data × gender) for South West; $S_2 \times S_4 \times G$ (DIP prison data × DIP community data × gender) for West Midlands; and $S_1 \times S_2 \times G$ (probation × DIP prison data × gender) for Yorkshire and Humber. For all interactions identified, females had an increased probability of being observed by both of the given sources. However identifying additional higher-order interactions for the regions (except London) did not appear to have a significant impact on the estimated population sizes, as noted above, yet did generally improve the goodness of fit to the observed data.

5. Discussion

Estimating the number of IDUs and the injecting DRD rate is an inherently difficult problem due to injecting as an ostracized behaviour and yet injectors' have a clear social and economic impact within society. The use of data from capture-recapture studies for estimating such hidden populations has a long history. The use of log-linear models is appealing due to their direct modelling (and interpretation) of interactions between the different data sources and/or covariates which are likely to be present within such complex systems. The corresponding estimates of IDU prevalence are model-dependent. We implement a model-averaging approach to take into account both parameter and model uncertainty within the estimation of population size, although there can still be dependency on the set of possible models considered.

The estimated total IDU population size in England of approximately 200,000 in 2005/6 is broadly consistent with the previous estimate obtained by de Angelis *et al* (2009) when investigating HCV prevalence, but has considerably less uncertainty associated with it. Our analysis also provides a regional dimension, offering new insights into injecting DRD rates regionally, and to regional interactions between sources.

Providing regional cross-classified estimates of IDUs and injecting DRD rates gives more detailed information that may be useful in assessing the regional impact of OST in reducing mortality risk. In addition, transmission risk for blood-borne viruses may be better assessed for different cross-categories at the regional level, by providing estimates of potential carriers. Besides providing regional estimates of IDUs, regional differences in terms of the underlying interactions may be of interest because they provide insight into cross-linkages between the different data sources and/or covariates.

Due to the structure of the data, which allows for age-group and gender as covariates, population estimates can be obtained at these lower cross-classification levels within each region, and permit the identification of more complex underlying structure and/or patterns.

For example, for both male and female IDUs in the North East, an unusually high proportion are younger individuals (15-34) with posterior means for the ratio of younger to older IDUs greater than 4 (see Table 4). We also note that, consistently within each region, and aggregated to the England level, the younger to older ratio is higher for females than males, indicating that a larger proportion of younger IDUs are female than of older IDUs. The higher proportion of younger female IDUs was also observed by King *et al* (2009) within Scotland. We note that, in this analysis, the capture-recapture data for each region were assumed to be independent of each other. It is possible to consider a single integrated analysis with the region itself as a categorical covariate within the analysis, with each level of the covariate corresponding to each region, and once more allowing interactions between the different sources/covariates and region. This may potentially allow the borrowing of information across the different regions and is an area of current research.

The estimates of IDU prevalence can be combined with the number of injecting DRDs to obtain the injectors' drug-related mortality risk. Within our analysis, we take the number of injecting DRDs to be the average annual number of HRDs in each region which occurred over the four year period 2004-7. There is additional potential heterogeneity in terms of identifying and reporting illicit drugs in post-mortem examinations. The number of HRDs are used both for constructing a prior for the total population size and in calculating the injecting DRD rate, by combining the number of HRDs with the estimated number of IDUs. It is possible to consider adding a further level of uncertainty to the number of HRDs per region. This would widen the prior interval specified on the total population size, but would have little impact on the posterior estimates of prevalence of IDUs since the posterior distributions are largely data-driven (although doing so may create greater overlaps between the prior and posterior estimates of population size). Additionally, for each region, assuming a Poisson or negative binomial distribution, say, for the annual number of HRDs (with mean equal to the annual mean number of HRDs) would result in essentially the same posterior mean for the injecting DRD rate (assuming the posterior distribution for the total populations sizes are unchanged), but with a wider credible interval to reflect the additional level of uncertainty incorporated.

The generally lower injecting DRD rates for England than in Scotland (King *et al*, 2009) suggests that Scotland may have something to learn from the cross-linkages that England has put in place. Discussion of regional source $\times$ source interactions with regions' criminal justice or drug treatment practitioners may shed further light on regional implications when local expertise is brought to bear on their interpretation. This analysis appears to offer a broad reassurance that criminal justice and drug treatment interventions are working together. However, there are concerns also - particularly for those regions in which injector ratios by age-group (15-34 to 35-64) are high and thereby suggest an unwelcome preponderance of younger injectors, which means that greater resistance to injecting needs to be engendered in their young people.

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A. Alternative model parameterisation

An alternative parameterisation of the model specifies the total cell counts for each gender $\times$ age-group as explicit model parameters. Such a parameterisation may be desirable if there is expert prior information available at this level and the data themselves are not sufficiently informative. The corresponding log-linear parameters are the main effect terms for each source and two-way interactions for source $\times$ source and source $\times$ covariate combinations (the covariate-only log-linear parameters relating to main effect covariate terms and covariate $\times$ covariate interaction term are no longer strictly estimable). We let $\boldsymbol{N} = \{N_{(g,a)} : g \in \{M, F\}, a \in \{15-34, 35-64\}\}$ and $p_{\boldsymbol{k}|(g,a)}$ denote the probability that an individual is observed in cell $\boldsymbol{k} \in \{0,1\}^4$, conditional on being of gender g in age-group a. The saturated log-linear model (up to two-way interactions) for the conditional cell probabilities are given by,

$$p_{\boldsymbol{k}|(g,a)} \propto \exp\left(\sum_{i=1}^{4}\theta^{S_i}_{k(i)} + \sum_{i=1}^{3}\sum_{j=i+1}^{4}\theta^{S_i,S_j}_{k(i),k(j)} + \sum_{i=1}^{4}\theta^{S_i,G}_{k(i),g} + \sum_{i=1}^{4}\theta^{S_i,A}_{k(i),a}\right).$$

In addition, letting $\boldsymbol{n}_{(g,a)} = \{\boldsymbol{n}_{(g,a):\boldsymbol{k}} : \boldsymbol{k} \in \{0,1\}^4\}$, for each combination of gender g and age-group a,

$$\boldsymbol{n}_{(g,a)}|N_{(g,a)}, \boldsymbol{\theta}_m \sim \text{Multinomial}(N_{(g,a)}, \boldsymbol{p}_{(g,a)}),$$

where $\boldsymbol{p}_{(g,a)} = \{p_{\boldsymbol{k}|(g,a)} : \boldsymbol{k} \in \{0,1\}^4\}$. The posterior distribution of the model parameters is given by,

$$\begin{aligned}
\pi(\boldsymbol{N}, \boldsymbol{\theta}_m|\boldsymbol{n}_{obs}) &\propto f(\boldsymbol{n}_{obs}|\boldsymbol{N}, \boldsymbol{\theta}_m)p(\boldsymbol{N}, \boldsymbol{\theta}_m) \\
&\propto \left[\prod_{g\in\{M,F\}}\prod_{a\in\{15-34,35-64\}} f(\boldsymbol{n}_{(g,a)}|N_{(g,a)}, \boldsymbol{\theta}_m)\right] p(\boldsymbol{N}, \boldsymbol{\theta}_m) \\
&\propto \left[\prod_{g\in\{M,F\}}\prod_{a\in\{15-34,35-64\}} \frac{N_{(g,a)}!}{n_{(g,a):\boldsymbol{0}}!}\prod_{\boldsymbol{k}\in\{0,1\}^4} p^{n_{(g,a):\boldsymbol{k}}}_{\boldsymbol{k}|(g,a)}\right] p(\boldsymbol{N}, \boldsymbol{\theta}_m).
\end{aligned}$$

We note that the priors are specified on the total population size for each gender $\times$ age-group cross-classification, i.e. $\boldsymbol{N}$ (and typically independently of $\boldsymbol{\theta}_m$). The corresponding MCMC algorithm would, for example, update each $N_{(g,a)}$ in turn using a Metropolis-Hastings step (analogous to that for N_{tot} in Section 3.4.1).

We note that prior information may not always be of the form of the total population size of each gender $\times$ age-group cross-classification, but functions of these. For example, prior information may be available on the total population size, male to female ratio (denoted R) and the proportion of males (and females) that are young (denoted by P_1 and P_2, respectively). Prior information of this form can be incorporated into this model parameterisation

by specifying a prior distribution on N_{tot}, R, P_1 and P_2, denoted by $p(N_{tot}, R, P_1, P_2)$ and calculating the corresponding prior on the total population counts for each gender $\times$ age-group cross-classification, denoted by $p(\boldsymbol{N})$, using a transformation of variables argument. For this example,

$$R = \frac{N_{(M)}}{N_{(F)}}, \qquad P_1 = \frac{N_{(M,15-34)}}{N_{(M)}} \qquad \text{and} \qquad P_2 = \frac{N_{(F,15-34)}}{N_{(F)}}.$$

Then, we can write,

$$p(\boldsymbol{N}) = p(N_{tot}, R, P_1, P_2) \left| \frac{d(N_{tot}, R, P_1, P_2)}{d\boldsymbol{N}} \right|,$$

where the final term corresponds to the determinant of the Jacobian. It is straightforward to show that,

$$\begin{aligned} \left| \frac{d(N_{tot}, R, P_1, P_2)}{d\boldsymbol{N}} \right| &= \begin{vmatrix} 1 & 1 & 1 & 1 \\ \frac{1}{N_{(M)}} - \frac{N_{(M,15-34)}}{N_{(M)}^2} & -\frac{N_{(M,15-34)}}{N_{(M)}^2} & 0 & 0 \\ \frac{1}{N_{(F)}} & \frac{1}{N_{(F)}} & -\frac{N_{(M)}}{N_{(F)}^2} & -\frac{N_{(M)}}{N_{(F)}^2} \\ 0 & 0 & \frac{1}{N_{(F)}} - \frac{N_{(F,15-34)}}{N_{(F)}^2} & -\frac{N_{(F,15-34)}}{N_{(F)}^2} \end{vmatrix} \\ &= \frac{N_{tot}}{N_{(M)} N_{(F)}^3}. \end{aligned}$$

In general, such results are easily obtained using an algebraic computer package, such as Maple.

Finally, we note that further parameterisations are possible which may be suitable for different prior information. For example, following on from the prior specification above, if there is expert prior information on only N_{tot} and R, it is possible to express the likelihood of observed data given the total number of males and total number of females using an analogous approach, conditioning on gender only (instead of gender and age-group as above). The log-linear parameter corresponding to the main effect term for gender is no longer estimable, but the rest of the covariate (and source) log-linear parameters are.

B. Data

The observed contingency tables for each region, cross-classified by gender and age are provided. The four sources correspond to,

$S1$ = Probation data;

$S2$ = Drug Intervention Programme (DIP) prison assessments;

$S3$ = Drug treatment data;

$S4$ = Drug Intervention Programme (DIP) community assessments.

Note that small observed cell sizes (entries < 5) have been replaced by a * to comply with the Home Office request relating to avoiding potential deductive disclosure.

Table 7. Counts for East England

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	184	58	89	29
0	1	0	0	85	6	36	*
1	1	0	0	9	*	*	*
0	0	1	0	912	422	673	209
1	0	1	0	98	31	46	13
0	1	1	0	19	5	6	*
1	1	1	0	5	*	*	*
0	0	0	1	166	43	67	8
1	0	0	1	24	7	13	*
0	1	0	1	6	*	*	*
1	1	0	1	*	*	*	*
0	0	1	1	41	21	16	*
1	0	1	1	10	6	6	*
0	1	1	1	9	*	*	*
1	1	1	1	*	*	*	*
			Totals	1574	605	962	267

Table 8. Counts for East Midlands

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	299	66	81	14
0	1	0	0	205	8	35	*
1	1	0	0	31	*	*	*
0	0	1	0	1769	651	749	220
1	0	1	0	226	64	51	9
0	1	1	0	60	*	13	*
1	1	1	0	26	*	6	*
0	0	0	1	308	72	80	9
1	0	0	1	37	7	6	*
0	1	0	1	21	*	*	*
1	1	0	1	8	*	*	*
0	0	1	1	267	64	73	16
1	0	1	1	80	21	16	*
0	1	1	1	21	*	*	*
1	1	1	1	7	*	*	*
			Totals	3365	963	1117	272

Table 9. Counts for London

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	121	30	125	20
0	1	0	0	127	33	90	6
1	1	0	0	7	*	5	*
0	0	1	0	1554	752	2582	789
1	0	1	0	28	14	44	5
0	1	1	0	33	6	23	8
1	1	1	0	8	*	*	*
0	0	0	1	557	144	397	84
1	0	0	1	16	5	12	*
0	1	0	1	21	5	11	*
1	1	0	1	*	*	*	*
0	0	1	1	184	62	171	37
1	0	1	1	8	*	11	*
0	1	1	1	20	*	19	*
1	1	1	1	*	*	*	*
		Totals		2687	1062	3492	957

Table 10. Counts for North East

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	228	74	47	7
0	1	0	0	135	17	21	*
1	1	0	0	18	*	*	*
0	0	1	0	1778	584	465	122
1	0	1	0	242	63	35	5
0	1	1	0	55	12	9	*
1	1	1	0	30	9	*	*
0	0	0	1	189	35	17	*
1	0	0	1	24	*	*	*
0	1	0	1	10	*	*	*
1	1	0	1	5	*	*	*
0	0	1	1	145	35	21	*
1	0	1	1	60	17	12	*
0	1	1	1	13	*	5	*
1	1	1	1	12	*	*	*
		Totals		2944	858	643	140

Table 11. Counts for North West

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	390	113	238	58
0	1	0	0	167	25	73	11
1	1	0	0	21	*	6	*
0	0	1	0	2736	1231	2797	775
1	0	1	0	229	85	166	25
0	1	1	0	52	7	21	*
1	1	1	0	20	5	*	*
0	0	0	1	457	144	272	54
1	0	0	1	63	13	43	9
0	1	0	1	31	5	9	*
1	1	0	1	9	*	*	*
0	0	1	1	323	86	215	25
1	0	1	1	139	32	47	8
0	1	1	1	33	5	7	*
1	1	1	1	8	*	*	*
		Totals		4678	1756	3904	971

Table 12. Counts for South East

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	246	99	123	30
0	1	0	0	96	24	31	*
1	1	0	0	18	*	*	*
0	0	1	0	1609	648	1101	322
1	0	1	0	160	45	83	14
0	1	1	0	43	*	13	*
1	1	1	0	17	*	*	*
0	0	0	1	267	69	94	17
1	0	0	1	11	7	5	*
0	1	0	1	*	*	*	*
1	1	0	1	*	*	*	*
0	0	1	1	107	33	36	8
1	0	1	1	18	5	8	*
0	1	1	1	5	*	*	*
1	1	1	1	*	*	*	*
		Totals		2605	940	1498	401

Table 13. Counts for South West

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	146	35	61	6
0	1	0	0	120	26	46	*
1	1	0	0	16	*	*	*
0	0	1	0	3151	1377	2075	659
1	0	1	0	206	63	66	11
0	1	1	0	90	13	18	*
1	1	1	0	24	*	5	*
0	0	0	1	120	21	45	*
1	0	0	1	12	*	5	*
0	1	0	1	*	*	*	*
1	1	0	1	*	*	*	*
0	0	1	1	159	30	73	6
1	0	1	1	29	9	5	*
0	1	1	1	13	*	*	*
1	1	1	1	*	*	*	*
		Totals		4091	1580	2405	691

Table 14. Counts for West Midlands

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	277	69	77	22
0	1	0	0	225	24	43	5
1	1	0	0	34	*	7	*
0	0	1	0	2252	780	958	259
1	0	1	0	239	36	58	11
0	1	1	0	92	9	10	*
1	1	1	0	53	6	6	*
0	0	0	1	312	67	68	11
1	0	0	1	44	7	15	*
0	1	0	1	37	5	*	*
1	1	0	1	10	*	*	*
0	0	1	1	199	45	59	13
1	0	1	1	68	15	21	*
0	1	1	1	23	8	*	*
1	1	1	1	21	*	*	*
		Totals		3886	1081	1332	328

Table 15. Counts for Yorkshire

S1	S2	S3	S4	Male 15-34	Female 15-34	Male 35-64	Female 35-64
1	0	0	0	372	139	133	24
0	1	0	0	196	23	43	*
1	1	0	0	18	9	*	*
0	0	1	0	3604	1481	1388	378
1	0	1	0	364	109	95	20
0	1	1	0	99	13	14	*
1	1	1	0	36	7	*	*
0	0	0	1	676	193	174	28
1	0	0	1	100	16	27	6
0	1	0	1	41	9	5	*
1	1	0	1	10	*	*	*
0	0	1	1	538	150	144	28
1	0	1	1	281	58	46	5
0	1	1	1	52	*	8	*
1	1	1	1	26	9	7	*
		Totals		6413	2221	2089	498

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